

## SEQUENCE LISTING

<110> ALBANI, SALVATORE

<120> METHOD FOR ISOLATION, QUANTIFICATION, CHARACTERIZATION  
AND MODULATION OF ANTIGEN-SPECIFIC T CELLS

<130> AND-TCCCIPI-DIV1

<140>

<141>

<150> 09/756,983

<151> 2001-01-09

<150> PCT/US99/24666

<151> 1999-10-19

<150> 09/421,506

<151> 1999-10-19

<150> 60/105,018

<151> 1998-10-20

<160> 24

<170> PatentIn Ver. 2.1

<210> 1

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide derived  
from third hyper V region of IE molecule of *Mus musculus*

<400> 1

Ala Ser Phe Glu Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys  
1 5 10 15

Ala

<210> 2

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide derived  
from bole I protein of Epstein Barr virus

<400> 2

Thr Arg Asp Asp Ala Glu Tyr Leu Leu Gly Arg Glu Ser Val Leu  
1 5 10 15

<210> 3  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic peptide derived from the haemophilus influenza virus

<400> 3  
Thr Ser Phe Pro Met Arg Gly Asp Leu Ala Lys Arg Glu Pro Asp Lys  
1 5 10 15

<210> 4  
<211> 36  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic peptide derived from the TCR receptor of Mus musculus

<220>  
<221> MOD\_RES  
<222> (18)  
<223> Ser, Ile or Thr

<400> 4  
Leu His Ile Ser Ala Val Asp Pro Glu Asp Ser Ala Val Tyr Phe Cys  
1 5 10 15

Ala Xaa Ser Gln Glu Phe Phe Ser Ser Tyr Glu Gln Tyr Phe Gly Pro  
20 25 30

Gly Thr Arg Leu  
35

<210> 5  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic peptide derived from the influenza virus

<400> 5  
Gly Ile Leu Gly Phe Val Phe Thr Leu  
1 5

<210> 6  
<211> 9  
<212> PRT  
<213> Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic peptide derived  
from the influenza virus

&lt;400&gt; 6

Val Lys Leu Gly Glu Phe Tyr Asn Gln  
1 5

&lt;210&gt; 7

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Synthetic peptide

&lt;220&gt;

&lt;221&gt; MOD\_RES

&lt;222&gt; (2)

&lt;223&gt; cyclohexylalanine

&lt;400&gt; 7

Lys Xaa Val Ala Ala Trp Thr Leu Lys Ala Ala  
1 5 10

&lt;210&gt; 8

&lt;211&gt; 13

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic peptide derived  
from the influenza virus

&lt;400&gt; 8

Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr  
1 5 10

&lt;210&gt; 9

&lt;211&gt; 17

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Artificial

&lt;400&gt; 9

Ile Ser Gln Ala Val His Ala Ala His Ala Glu Ile Asn Glu Ala Gly  
1 5 10 15

Arg

<210> 10  
<211> 15  
<212> PRT  
<213> Escherichia coli

<400> 10  
Gln Lys Arg Ala Ala Tyr Asp Gln Tyr Gly His Ala Ala Phe Glu  
1 5 10 15

<210> 11  
<211> 15  
<212> PRT  
<213> Homo sapiens

<400> 11  
Gln Lys Arg Ala Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly  
1 5 10 15

<210> 12  
<211> 9  
<212> PRT  
<213> Homo sapiens

<400> 12  
Gly Ile Leu Gly Phe Val Phe Thr Leu  
1 5

<210> 13  
<211> 9  
<212> PRT  
<213> Homo sapiens

<400> 13  
Val Lys Leu Gly Glu Phe Tyr Asn Gln  
1 5

<210> 14  
<211> 13  
<212> PRT  
<213> Homo sapiens

<400> 14  
Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr  
1 5 10

<210> 15  
<211> 942  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Fusion construct with  
human and bacterial sequences

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(939)

&lt;400&gt; 15

atg	gac	cac	aca	cgg	agg	cag	gga	aca	tca	cca	tcc	aag	tgt	cca	tac	48
Met	Gly	His	Thr	Arg	Arg	Gln	Gly	Thr	Ser	Pro	Ser	Lys	Cys	Pro	Tyr	
1	5							10							15	

ctc	aat	ttc	ttt	cag	ctc	ttg	gtg	ctg	gct	ggt	ctt	tct	cac	ttc	tgt	96
Leu	Asn	Phe	Phe	Gln	Leu	Leu	Val	Leu	Ala	Gly	Leu	Ser	His	Phe	Cys	
20					25							30				

tca	ggt	gtt	atc	cac	gtg	acc	aag	gaa	gtg	aaa	gaa	gtg	gca	acg	ctg	144
Ser	Gly	Val	Ile	His	Val	Thr	Lys	Glu	Val	Lys	Glu	Val	Ala	Thr	Leu	
35						40							45			

tcc	tgt	ggt	cac	aat	gtt	tct	gtt	gaa	gag	ctg	gca	caa	act	cgc	atc	192
Ser	Cys	Gly	His	Asn	Val	Ser	Val	Glu	Glu	Leu	Ala	Gln	Thr	Arg	Ile	
50					55							60				

tac	tgg	caa	aag	gag	aag	aaa	atg	gtg	ctg	act	atg	atg	tct	ggg	gac	240
Tyr	Trp	Gln	Lys	Glu	Lys	Met	Val	Leu	Thr	Met	Met	Ser	Gly	Asp		
65					70						75			80		

atg	aat	ata	tgg	ccc	gag	tac	aag	aac	cgg	acc	atc	ttt	gat	atc	act	288
Met	Asn	Ile	Trp	Pro	Glu	Tyr	Lys	Asn	Arg	Thr	Ile	Phe	Asp	Ile	Thr	
						85				90			95			

aat	aac	ctc	tcc	att	gtg	atc	ctg	gct	ctg	cgc	cca	tct	gac	gag	ggc	336
Asn	Asn	Leu	Ser	Ile	Val	Ile	Leu	Ala	Leu	Arg	Pro	Ser	Asp	Glu	Gly	
						100			105			110				

aca	tac	gag	tgt	gtt	ctg	aag	tat	gaa	aaa	gac	gct	ttc	aag	cgg	384	
Thr	Tyr	Glu	Cys	Val	Val	Leu	Lys	Tyr	Glu	Lys	Asp	Ala	Phe	Lys	Arg	
						115		120		125						

gaa	cac	ctg	gct	gaa	gtg	acg	tta	tca	gtc	aaa	gct	gac	ttc	cct	aca	432
Glu	His	Leu	Ala	Glu	Val	Thr	Leu	Ser	Val	Lys	Ala	Asp	Phe	Pro	Thr	
						130		135		140						

cct	agt	ata	tct	gac	ttt	gaa	att	cca	act	tct	aat	att	aga	agg	ata	480
Pro	Ser	Ile	Ser	Asp	Phe	Glu	Ile	Pro	Thr	Ser	Asn	Ile	Arg	Arg	Ile	
						145		150		155		160				

att	tgc	tca	acc	tct	gga	ggt	ttt	cca	gag	cct	cac	ctc	tcc	tgg	ttg	528
Ile	Cys	Ser	Thr	Ser	Gly	Gly	Phe	Pro	Glu	Pro	His	Leu	Ser	Trp	Leu	
						165		170		175						

gaa	aat	gga	gaa	gaa	tta	aat	gcc	atc	aac	aca	aca	gtt	tcc	caa	gat	576
Glu	Asn	Gly	Glu	Glu	Leu	Asn	Ala	Ile	Asn	Thr	Thr	Val	Ser	Gln	Asp	
						180		185		190						

cct	gaa	act	gag	ctc	tat	gct	gtt	agc	gaa	ttc	ggc	ggc	tcc	ggt	ggt	624
Pro	Glu	Thr	Glu	Leu	Tyr	Ala	Val	Ser	Glu	Phe	Gly	Gly	Ser	Gly	Gly	
						195		200		205						

agc gcc aca cct caa aat att act gat ttg tgt gca gaa tac cac aac Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu Cys Ala Glu Tyr His Asn	672
210 215 220	
aca caa ata cat acg cta aat gat aag ata ttt tcg tat aca gaa tct Thr Gln Ile His Thr Leu Asn Asp Lys Ile Phe Ser Tyr Thr Glu Ser	720
225 230 235 240	
cta gct gga aaa aga gag atg gct atc att act ttt aag aat ggt gca Leu Ala Gly Lys Arg Glu Met Ala Ile Ile Thr Phe Lys Asn Gly Ala	768
245 250 255	
act ttt caa gta gaa gta cca ggt agt caa cat ata gat tca caa aaa Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp Ser Gln Lys	816
260 265 270	
aaa gcg att gaa agg atg aag gat acc ctg agg att gca tat ctt act Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Ala Tyr Leu Thr	864
275 280 285	
gaa gct aaa gtc gaa aag tta tgt gta tgg aat aat aaa acg cct cat Glu Ala Lys Val Glu Lys Leu Cys Val Trp Asn Asn Lys Thr Pro His	912
290 295 300	
gcg att gcc gca att agt atg gca aat taa Ala Ile Ala Ala Ile Ser Met Ala Asn	942
305 310	

<210> 16  
 <211> 313  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fusion construct with  
 human and bacterial sequences

<400> 16  
 Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr  
 1 5 10 15  
 Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys  
 20 25 30  
 Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu  
 35 40 45  
 Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile  
 50 55 60  
 Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp  
 65 70 75 80  
 Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr  
 85 90 95

Asn	Asn	Leu	Ser	Ile	Val	Ile	Leu	Ala	Leu	Arg	Pro	Ser	Asp	Glu	Gly
100							105						110		
Thr	Tyr	Glu	Cys	Val	Val	Leu	Lys	Tyr	Glu	Lys	Asp	Ala	Phe	Lys	Arg
115						120						125			
Glu	His	Leu	Ala	Glu	Val	Thr	Leu	Ser	Val	Lys	Ala	Asp	Phe	Pro	Thr
130						135					140				
Pro	Ser	Ile	Ser	Asp	Phe	Glu	Ile	Pro	Thr	Ser	Asn	Ile	Arg	Arg	Ile
145						150					155		160		
Ile	Cys	Ser	Thr	Ser	Gly	Gly	Phe	Pro	Glu	Pro	His	Leu	Ser	Trp	Leu
165							170					175			
Glu	Asn	Gly	Glu	Glu	Leu	Asn	Ala	Ile	Asn	Thr	Thr	Val	Ser	Gln	Asp
180							185					190			
Pro	Glu	Thr	Glu	Leu	Tyr	Ala	Val	Ser	Glu	Phe	Gly	Gly	Ser	Gly	Gly
195							200					205			
Ser	Ala	Thr	Pro	Gln	Asn	Ile	Thr	Asp	Leu	Cys	Ala	Glu	Tyr	His	Asn
210						215					220				
Thr	Gln	Ile	His	Thr	Leu	Asn	Asp	Lys	Ile	Phe	Ser	Tyr	Thr	Glu	Ser
225						230					235		240		
Leu	Ala	Gly	Lys	Arg	Glu	Met	Ala	Ile	Ile	Thr	Phe	Lys	Asn	Gly	Ala
245							250					255			
Thr	Phe	Gln	Val	Glu	Val	Pro	Gly	Ser	Gln	His	Ile	Asp	Ser	Gln	Lys
260						265					270				
Lys	Ala	Ile	Glu	Arg	Met	Lys	Asp	Thr	Leu	Arg	Ile	Ala	Tyr	Leu	Thr
275						280					285				
Glu	Ala	Lys	Val	Glu	Lys	Leu	Cys	Val	Trp	Asn	Asn	Lys	Thr	Pro	His
290						295					300				
Ala	Ile	Ala	Ala	Ile	Ser	Met	Ala	Asn							
305						310									

&lt;210&gt; 17

&lt;211&gt; 1056

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Fusion construct with human and bacterial sequences

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1053)

<400> 17  
 atg gga ctg agt aac att ctc ttt gtg atg gcc ttc ctg ctc tct ggt 48  
 Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu Leu Ser Gly  
 1 5 10 15

gct gct cct ctg aag att caa gct tat ttc aat gag act gca gac ctg 96  
 Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu  
 20 25 30

cca tgc caa ttt gca aac tct caa aac caa agc ctg agt gag cta gta 144  
 Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser Glu Leu Val  
 35 40 45

gta ttt tgg cag gac cag gaa aac ttg gtt ctg aat gag gta tac tta 192  
 Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu  
 50 55 60

ggc aaa gag aaa ttt gac agt gtt cat tcc aag tat atg ggc cgc aca 240  
 Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr  
 65 70 75 80

agt ttt gat tcg gac agt tgg acc ctg aga ctt cac aat ctt cag atc 288  
 Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn Leu Gln Ile  
 85 90 95

aag gac aag ggc ttg tat caa tgt atc atc cat cac aaa aag ccc aca 336  
 Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys Pro Thr  
 100 105 110

gga atg att cgc atc cac cag atg aat tct gaa ctg tca gtg ctt gct 384  
 Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala  
 115 120 125

aac ttc agt caa cct gaa ata gta cca att tct aat ata aca gaa aat 432  
 Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile Thr Glu Asn  
 130 135 140

gtg tac ata aat ttg acc tgc tca tct ata cac ggt tac cca gaa cct 480  
 Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr Pro Glu Pro  
 145 150 155 160

aag aag atg agt gtt ttg cta aga acc aag aat tca act atc gag tat 528  
 Lys Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr Ile Glu Tyr  
 165 170 175

gat ggt att atg cag aaa tct caa gat aat gtc aca gaa ctg tac gac 576  
 Asp Gly Ile Met Gln Lys Ser Gln Asp Asn Val Thr Glu Leu Tyr Asp  
 180 185 190

gtt tcc atc agc ttg tct gtt tca ttc cct gat gtt acg agc aat atg 624  
 Val Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr Ser Asn Met  
 195 200 205

acc atc ttc tgt att ctg gaa act gac aag acg cgg ctt tta tct tca 672  
 Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu Leu Ser Ser  
 210 215 220

cct ttc tct ata gag ctt gag gac cct cag cct ccc cca gac cac gaa	720
Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro Asp His Glu	
225 230 235 240	
ttc ggc ggc tcc ggt ggt agc gcc aca cct caa aat att act gat ttg	768
Phe Gly Gly Ser Gly Gly Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu	
245 250 255	
tgt gca gaa tac cac aac aca caa ata cat acg cta aat gat aag ata	816
Cys Ala Glu Tyr His Asn Thr Gln Ile His Thr Leu Asn Asp Lys Ile	
260 265 270	
ttt tcg tat aca gaa tct cta gct gga aaa aga gag atg gct atc att	864
Phe Ser Tyr Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile Ile	
275 280 285	
act ttt aag aat ggt gca act ttt caa gta gaa gta cca ggt agt caa	912
Thr Phe Lys Asn Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln	
290 295 300	
cat ata gat tca caa aaa aaa gcg att gaa agg atg aag gat acc ctg	960
His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu	
305 310 315 320	
agg att gca tat ctt act gaa gct aaa gtc gaa aag tta tgt gta tgg	1008
Arg Ile Ala Tyr Leu Thr Glu Ala Lys Val Glu Lys Leu Cys Val Trp	
325 330 335	
aat aat aaa acg cct cat gcg att gcc gca att agt atg gca aat taa	1056
Asn Asn Lys Thr Pro His Ala Ile Ala Ala Ile Ser Met Ala Asn	
340 345 350	

&lt;210&gt; 18

&lt;211&gt; 351

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Fusion construct with human and bacterial sequences

&lt;400&gt; 18

Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu Leu Ser Gly

1 5 10 15

Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu

20 25 30

Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser Glu Leu Val

35 40 45

Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu

50 55 60

Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr

65 70 75 80

Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn Leu Gln Ile  
 85 90 95  
 Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys Lys Pro Thr  
 100 105 110  
 Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala  
 115 120 125  
 Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile Thr Glu Asn  
 130 135 140  
 Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr Pro Glu Pro  
 145 150 155 160  
 Lys Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr Ile Glu Tyr  
 165 170 175  
 Asp Gly Ile Met Gln Lys Ser Gln Asp Asn Val Thr Glu Leu Tyr Asp  
 180 185 190  
 Val Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr Ser Asn Met  
 195 200 205  
 Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu Leu Ser Ser  
 210 215 220  
 Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro Asp His Glu  
 225 230 235 240  
 Phe Gly Gly Ser Gly Gly Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu  
 245 250 255  
 Cys Ala Glu Tyr His Asn Thr Gln Ile His Thr Leu Asn Asp Lys Ile  
 260 265 270  
 Phe Ser Tyr Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile Ile  
 275 280 285  
 Thr Phe Lys Asn Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln  
 290 295 300  
 His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu  
 305 310 315 320  
 Arg Ile Ala Tyr Leu Thr Glu Ala Lys Val Glu Lys Leu Cys Val Trp  
 325 330 335  
 Asn Asn Lys Thr Pro His Ala Ile Ala Ala Ile Ser Met Ala Asn  
 340 345 350

<210> 19  
<211> 31  
<212> PRT  
<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Synthetic peptide

&lt;400&gt; 19

Ser Ala Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Asn Ala  
1 5 10 15Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Leu Ala Gln  
20 25 30

&lt;210&gt; 20

&lt;211&gt; 30

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Synthetic peptide

&lt;400&gt; 20

Ala Gln Leu Lys Lys Lys Leu Gln Ala Leu Lys Lys Lys Asn Ala Gln  
1 5 10 15Leu Lys Gln Lys Leu Gln Ala Leu Lys Lys Lys Leu Ala Gln  
20 25 30

&lt;210&gt; 21

&lt;211&gt; 1095

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Fusion construct with  
human and bacterial sequences

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1092)

&lt;400&gt; 21

atg gcc ata agt gga gtc cct gtg cta gga ttt ttc atc ata gct gtg 48  
Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val  
1 5 10 15ctg atg agc gct cag gaa tca tgg gct atc aaa gaa gaa cat gtg atc 96  
Leu Met Ser Ala Gln Glu Ser Trp Ala Ile Lys Glu Glu His Val Ile  
20 25 30atc cag gcc gag ttc tat ctg aat cct gac caa tca ggc gag ttt atg 144  
Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met  
35 40 45ttt gac ttt gat ggt gat gag att ttc cat gtg gat atg gca aag aag 192  
Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys  
50 55 60

gag acg gtc tgg cgg ctt gaa gaa ttt gga cga ttt gcc agc ttt gag	240
Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu	
65 70 75 80	
gct caa ggt gca ttg gcc aac ata gct gtg gac aaa gcc aac ctg gaa	288
Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu	
85 90 95	
atc atg aca aag cgc tcc aac tat act ccg atc acc aat gta cct cca	336
Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro	
100 105 110	
gag gta act gtg ctc acg aac agc cct gtg gaa ctg aga gag ccc aac	384
Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn	
115 120 125	
gtc ctc atc tgt ttc atc gac aag ttc acc cca cca gtg gtc aat gtc	432
Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val	
130 135 140	
acg tgg ctt cga aat gga aaa cct gtc acc aca gga gtg tca gag aca	480
Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr	
145 150 155 160	
gtc ttc ctg ccc agg gaa gac cac ctt ttc cgc aag ttc cac tat ctc	528
Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu	
165 170 175	
ccc ttc ctg ccc tca act gag gac gtt tac gac tgc agg gtg gag cac	576
Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His	
180 185 190	
tgg ggc ttg gat gag cct ctt ctc aag cac tgg gag ttt gat gct cca	624
Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro	
195 200 205	
agc cct ctc cca gag act aca gag gaa ttc ggt ggt tcc ggt ggt tcc	672
Ser Pro Leu Pro Glu Thr Thr Glu Glu Phe Gly Gly Ser Gly Gly Ser	
210 215 220	
gcg cag ctg gaa tgg gaa ctg cag gcg ctg gaa aaa gaa aac gcg cag	720
Ala Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Asn Ala Gln	
225 230 235 240	
ctg gaa tgg gaa ctg cag gcg ctg gaa aaa gaa ctg gcg cag ggc ggc	768
Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Leu Ala Gln Gly Gly	
245 250 255	
tcc ggt ggt agc gcc aca cct caa aat att act gat ttg tgt gca gaa	816
Ser Gly Gly Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu Cys Ala Glu	
260 265 270	
tac cac aac aca caa ata cat acg cta aat gat aag ata ttt tcg tat	864
Tyr His Asn Thr Gln Ile His Thr Leu Asn Asp Lys Ile Phe Ser Tyr	
275 280 285	

aca gaa tct cta gct gga aaa aga gag atg gct atc att act ttt aag	912
Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile Ile Thr Phe Lys	
290 295 300	
aat ggt gca act ttt caa gta gaa gta cca ggt agt caa cat ata gat	960
Asn Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp	
305 310 315 320	
tca caa aaa aaa gcg att gaa agg atg aag gat acc ctg agg att gca	1008
Ser, Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Ala	
325 330 335	
tat ctt act gaa gct aaa gtc gaa aag tta tgt gta tgg aat aat aaa	1056
Tyr Leu Thr Glu Ala Lys Val Glu Lys Leu Cys Val Trp Asn Asn Lys	
340 345 350	
acg cct cat gcg att gcc gca att agt atg gca aat taa	1095
Thr Pro His Ala Ile Ala Ala Ile Ser Met Ala Asn	
355 360	)

&lt;210&gt; 22

&lt;211&gt; 364

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Fusion construct with human and bacterial sequences

&lt;400&gt; 22

Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val  
1 5 10 15Leu Met Ser Ala Gln Glu Ser Trp Ala Ile Lys Glu Glu His Val Ile  
20 25 30Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met  
35 40 45Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys  
50 55 60Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu  
65 70 75 80Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu  
85 90 95Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro  
100 105 110Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn  
115 120 125Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val  
130 135 140

Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr  
 145 150 155 160  
 Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu  
 165 170 175  
 Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His  
 180 185 190  
 Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro  
 195 200 205  
 Ser Pro Leu Pro Glu Thr Thr Glu Glu Phe Gly Gly Ser Gly Gly Ser  
 210 215 220  
 Ala Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Asn Ala Gln  
 225 230 235 240  
 Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Leu Ala Gln Gly Gly  
 245 250 255  
 Ser Gly Gly Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu Cys Ala Glu  
 260 265 270  
 Tyr His Asn Thr Gln Ile His Thr Leu Asn Asp Lys Ile Phe Ser Tyr  
 275 280 285  
 Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile Ile Thr Phe Lys  
 290 295 300  
 Asn Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp  
 305 310 315 320  
 Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Ala  
 325 330 335  
 Tyr Leu Thr Glu Ala Lys Val Glu Lys Leu Cys Val Trp Asn Asn Lys  
 340 345 350  
 Thr Pro His Ala Ile Ala Ala Ile Ser Met Ala Asn  
 355 360

<210> 23  
 <211> 861  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fusion construct with  
 human and bacterial sequences

<220>  
 <221> CDS  
 <222> (1)...(855)

<400> 23

atg gtg tgt ctg aag ttc cct gga ggc tcc tgc atg gca gct ctg aca	48
Met Val Cys Leu Lys Phe Pro Gly Gly Ser Cys Met Ala Ala Leu Thr	
1 5 10 15	
gtg aca ctg atg gtg ctg agc tcc cca ctg gct ttg gct ggg gac acc	96
Val Thr Leu Met Val Leu Ser Ser Pro Leu Ala Leu Ala Gly Asp Thr	
20 25 30	
cga cca cgt ttc ttg gag cag gtt aaa cat gag tgt cat ttc ttc aac	144
Arg Pro Arg Phe Leu Glu Gln Val Lys His Glu Cys His Phe Phe Asn	
35 40 45	
ggg acg gag cgg gtg cgg ttc ctg gac aga tac ttc tat cac caa gag	192
Gly Thr Glu Arg Val Arg Phe Leu Asp Arg Tyr Phe Tyr His Gln Glu	
50 55 60	
gag tac gtg cgc ttc gac agc gac gtg ggg gag tac cgg gcg gtg acg	240
Glu Tyr Val Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr	
65 70 75 80	
gag ctg ggg cgg cct gat gcc gag tac tgg aac agc cag aag gac ctc	288
Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Lys Asp Leu	
85 90 95	
ctg gag cag aag cgg gcc gcg gtg gac acc tac tgc aga cac aac tac	336
Leu Glu Gln Lys Arg Ala Ala Val Asp Thr Tyr Cys Arg His Asn Tyr	
100 105 110	
ggg gtt ggt gag agc ttc aca gtg cag cgg cga gtc tat cct gag gtg	384
Gly Val Gly Glu Ser Phe Thr Val Gln Arg Arg Val Tyr Pro Glu Val	
115 120 125	
act gtg tat cct gca aag acc cag ccc ctg cag cac cac aac ctc ctg	432
Thr Val Tyr Pro Ala Lys Thr Gln Pro Leu Gln His His Asn Leu Leu	
130 135 140	
gtc tgc tct gtg aat ggt ttc tat cca ggc agc att gaa gtc agg tgg	480
Val Cys Ser Val Asn Gly Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp	
145 150 155 160	
ttc cgg aac ggc cag gaa gag aag act ggg gtg gtg tcc aca ggc ctg	528
Phe Arg Asn Gly Gln Glu Lys Thr Gly Val Val Ser Thr Gly Leu	
165 170 175	
atc cag aat gga gac tgg acc ttc cag acc ctg gtg atg ctg gaa aca	576
Ile Gln Asn Gly Asp Trp Thr Phe Gln Thr Leu Val Met Leu Glu Thr	
180 185 190	
gtt cct cgg agt gga gag gtt tac acc tgc caa gtg gag cac cca agc	624
Val Pro Arg Ser Gly Glu Val Tyr Thr Cys Gln Val Glu His Pro Ser	
195 200 205	
ctg acg agc cct ctc aca gtg gaa tgg aga gca cgg tct gaa tct gca	672
Leu Thr Ser Pro Leu Thr Val Glu Trp Arg Ala Arg Ser Glu Ser Ala	
210 215 220	

cag agc aag ggc ggc tcc ggt ggt agc gcc cag ctg aag aag aaa ctc	720
Gln Ser Lys Gly Gly Ser Gly Gly Ser Ala Gln Leu Lys Lys Lys Leu	
225 230 235 240	
cag gct ctg aaa aaa aag aat gcc cag ctc aag cag aag ctg cag gcc	768
Gln Ala Leu Lys Lys Asn Ala Gln Leu Lys Gln Lys Leu Gln Ala	
245 250 255	
ctg aag aaa aag ctg gct cag ggt tcc ggt tcc gcg ggt ggt ggt	816
Leu Lys Lys Leu Ala Gln Gly Ser Gly Gly Ser Ala Gly Gly Gly	
260 265 270	
ttg aac gac atc ttc gaa gct cag aaa atc gaa tgg cac taataa	861
Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His	
275 280 285	

&lt;210&gt; 24

&lt;211&gt; 285

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Fusion construct with human and bacterial sequences

&lt;400&gt; 24

Met Val Cys Leu Lys Phe Pro Gly Gly Ser Cys Met Ala Ala Leu Thr  
1 5 10 15Val Thr Leu Met Val Leu Ser Ser Pro Leu Ala Leu Ala Gly Asp Thr  
20 25 30Arg Pro Arg Phe Leu Glu Gln Val Lys His Glu Cys His Phe Phe Asn  
35 40 45Gly Thr Glu Arg Val Arg Phe Leu Asp Arg Tyr Phe Tyr His Gln Glu  
50 55 60Glu Tyr Val Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr  
65 70 75 80Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Lys Asp Leu  
85 90 95Leu Glu Gln Lys Arg Ala Ala Val Asp Thr Tyr Cys Arg His Asn Tyr  
100 105 110Gly Val Gly Glu Ser Phe Thr Val Gln Arg Arg Val Tyr Pro Glu Val  
115 120 125Thr Val Tyr Pro Ala Lys Thr Gln Pro Leu Gln His His Asn Leu Leu  
130 135 140Val Cys Ser Val Asn Gly Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp  
145 150 155 160

Phe Arg Asn Gly Gln Glu Glu Lys Thr Gly Val Val Ser Thr Gly Leu  
165 170 175

Ile Gln Asn Gly Asp Trp Thr Phe Gln Thr Leu Val Met Leu Glu Thr  
180 185 190

Val Pro Arg Ser Gly Glu Val Tyr Thr Cys Gln Val Glu His Pro Ser  
195 200 205

Leu Thr Ser Pro Leu Thr Val Glu Trp Arg Ala Arg Ser Glu Ser Ala  
210 215 220

Gln Ser Lys Gly Gly Ser Gly Ser Ala Gln Leu Lys Lys Lys Leu  
225 230 235 240

Gln Ala Leu Lys Lys Asn Ala Gln Leu Lys Gln Lys Leu Gln Ala  
245 250 255

Leu Lys Lys Leu Ala Gln Gly Ser Gly Gly Ser Ala Gly Gly Gly  
260 265 270

Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His  
275 280 285